```
   1  TCTGGGAAGG AGGCCAGGAG TGGGGCAGGT CAACTGACTG GGAGCAGGGG
  51  ATCTGGGTTC CAAGAAGGAG TTGTGTTTGA GGTGGGGTCT GGGTCCTCGT
 101  GGAAGTCAGG ACTCCCAGGC AGAAAAGAGG CAGGCTGCAG GGAAGTAAGG
 151  AGGAGGCATG GCACCTTCTC ATCGGGCATC ACAGGTGGGG TTTTGCCCCA
 201  CCCCTGAACG CCCTCTGTGG CGCCTTCCAC CCACCTGTAG GCCCAGAAGG
 251  ATGTCGGTCT GCTACCGTCC CCCAGGGAAC GAGACACTGC TGAGCTGGAA
 301  GACTTCGCGG GCCACAGGCA CAGCCTTCCT GCTGCTGGCG GCGCTGCTGG
 351  GGCTGCCTGG CAACGGTTTC GTGGTGTGGA GCTTGGCGGG CTGGCGGCTT
 401  GCACGGGGGC GACCGCTGGC GGCAACGCTT GTGTTGCACC TGGCGCTGGC
 451  CGACGGCGCG GTGCTGCTGC TCACGCCGTT CTTTGTGGCC TTCCTGACCC
 501  GGCAGGCTTG GCCGCTGGGC CAGGCGGGCT GCAAGGCGGT GTACTACGTG
 551  TGCGCGCTCA GCATGTACGC CAGCGTGCTG CTCACCGGCC TGCTCAGCCT
 601  GCAGCGCTGC TTCGCAGTCA CCCGCCCCTT CCTGGCGCTT CGGCTGCGCA
 651  GCCCGGCCCT GGCCCGCCGC CTGCTGCTGG CGGTCTGGCT GGCCGCCCTG
 701  TTGCTCGCCG TCCCGGCCGC CGTCTACCGC CACCTGTGGA GGGACCGCGT
 751  ATGCCAGCTG TGCCACCCGT CGCCGGTCCA CGCCGCCGCC CACCTGAGCC
 801  TGGAGACTCT GACCGCTTTC GTGCTTCCTT TCGGGCTGAT GCTCGGCTGC
 851  TACAGCGTGA CGCTGGCACG GCTGCGGGGC GCCCGCTGGG GCTCCGGGCG
 901  GCACGGGGCG CGGGTGGGCC GGCTGGTGAG CGCCATCGTG CTTGCCTTCG
 951  GCTTGCTCTG GGCCCCCTAC CACGCAGTCA ACCTTCTGCA GGCGGTCGCA
1001  GCGCTGGCTC CACCGGAAGG GGCCTTGGCG AAGCTGGGCG GAGCCGGCCA
1051  GGCGGCGCGA GCGGGAACTA CGGCCTTGGC CTTCTTCAGT TCTAGCGTCA
1101  ACCCGGTGCT CTACGTCTTC ACCGCTGGAG ATCTGCTGCC CCGGGCAGGT
1151  CCCCGTTTCC TCACGCGGCT CTTCGAAGGC TCTGGGGAGG CCCGAGGGGG
1201  CGGCCGCTCT AGGGAAGGGA CCATGGAGCT CCGAACTACC CCTCAGCTGA
1251  AAGTGGTGGG GCAGGGCCGC GGCAATGGAG ACCCGGGGGG TGGGATGGAG
1301  AAGGACGGTC CGGAATGGGA CCTTTGACAG CAGACCCTAC AACCTGCTGC
1351  CCTTCCCTGT CCCTTTCCAC CCCCCACCCA CCCTCCAGAG GTCAGTGTTC
1401  TGGGACATTT GGGGACCCTT CTTTGACTAG AGTTTGGATC TGGCTGGGTA
1451  GGATTAGTAT ACACTTGGGG CAGGCCCAGG CTCCTCCAAA CTGAGGGATT
1501  ATGAGGGTGG TGATGGTCCC TGTTAAGGAC TATTGTGTGC TTGCAAGTTG
```

FIG.1

```
  1   MAPSHRASQV GFCPTPERPL WRLPPTCRPR RMSVCYRPPG NETLLSWKTS

 51   RATGTAFLLL AALLGLPGNG FVVWSLAGWR LARGRPLAAT LVLHLALADG

101   AVLLLTPFFV AFLTRQAWPL GQAGCKAVYY VCALSMYASV LLTGLLSLQR

151   CFAVTRPFLA LRLRSPALAR RLLLAVWLAA LLLAVPAAVY RHLWRDRVCQ

201   LCHPSPVHAA AHLSLETLTA FVLPFGLMLG CYSVTLARLR GARWGSGRHG

251   ARVGRLVSAI VLAFGLLWAP YHAVNLLQAV AALAPPEGAL AKLGGAGQAA

301   RAGTTALAFF SSSVNPVLYV FTAGDLLPRA GPRFLTRLFE GSGEARGGGR

351   SREGTMELRT TPQLKVVGQG RGNGDPGGGM EKDGPEWDL
```

FIG.2

●   ● 　 PCT/US99/26303

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```
          10              30              50
CTGGGAAGGAGGCCAGGAGTGGGGCAGGTCAACTGACTGGGAGCAGGGGATCTGGGTTCC

          70              90              110
AAGAAGGAGTTGTGTTTGAGGTGGGGTCTGGGTCCTCGTGGAAGTCAGGACTCCCAGGCA

          130             150             170
GAAAAGAGGCAGGCTGCAGGGAAGTAAGGAGGAGGCATGGCACCTTCTCATCGGGCATCA
                                        MetAlaProSerHisArgAlaSer

          190             210             230
CAGGTGGGGTTTTGCCCCACCCCTGAACGCCCTCTGTGGCGCCTTCCACCCACCTGTAGG
GlnValGlyPheCysProThrProGluArgProLeuTrpArgLeuProProThrCysArg

          250             270             290
CCCAGAAGGATGTCGGTCTGCTACCGTCCCCCAGGGAACGAGACACTGCTGAGCTGGAAG
ProArgArgMetSerValCysTyrArgProProGlyAsnGluThrLeuLeuSerTrpLys

          310             330             350
ACTTCGCGGGCCACAGGCACAGCCTTCCTGCTGCTGGCGGCGCTGCTGGGGCTGCCTGGC
ThrSerArgAlaThrGlyThrAlaPheLeuLeuLeuAlaAlaLeuLeuGlyLeuProGly

          370             390             410
AACGGTTTCGTGGTGTGGAGCTTGGCGGGCTGGCGGCTTGCACGGGGGCGACCGCTGGCG
AsnGlyPheValValTrpSerLeuAlaGlyTrpArgLeuAlaArgGlyArgProLeuAla

          430             450             470
GCAACGCTTGTGTTGCACCTGGCGCTGGCCGACGGCGCGGTGCTGCTGCTCACGCCGTTC
AlaThrLeuValLeuHisLeuAlaLeuAlaAspGlyAlaValLeuLeuLeuThrProPhe

          490             510             530
TTTGTGGCCTTCCTGACCCGGCAGGCTTGGCCGCTGGGCCAGGCGGGCTGCAAGGCGGTG
PheValAlaPheLeuThrArgGlnAlaTrpProLeuGlyGlnAlaGlyCysLysAlaVal

          550             570             590
TACTACGTGTGCGCGCTCAGCATGTACGCCAGCGTGCTGCTCACCGGCCTGCTCAGCCTG
TyrTyrValCysAlaLeuSerMetTyrAlaSerValLeuLeuThrGlyLeuLeuSerLeu

          610             630             650
CAGCGCTGCTTCGCAGTCACCCGCCCCCTTCCTGGCGCTTCGGCTGCGCAGCCCGGCCCTG
GlnArgCysPheAlaValThrArgProPheLeuAlaLeuArgLeuArgSerProAlaLeu

          670             690             710
GCCCGCCGCCTGCTGCTGGCGGTCTGGCTGGCCGCCCTGTTGCTCGCCGTCCCGGCCGCC
AlaArgArgLeuLeuLeuAlaValTrpLeuAlaAlaLeuLeuLeuAlaValProAlaAla

          730             750             770
GTCTACCGCCACCTGTGGAGGGACCGCGTATGCCAGCTGTGCCACCCGTCGCCGGTCCAC
ValTyrArgHisLeuTrpArgAspArgValCysGlnLeuCysHisProSerProValHis
```

FIG 3A

```
        790                   810                   830
GCCGCCGCCCACCTGAGCCTGGAGACTCTGACCGCTTTCGTGCTTCCTTTCGGGCTGATG
AlaAlaAlaHisLeuSerLeuGluThrLeuThrAlaPheValLeuProPheGlyLeuMet

        850                   870                   890
CTCGGCTGCTACAGCGTGACGCTGGCACGGCTGCGGGGCGCCCGCTGGGGCTCCGGGCGG
LeuGlyCysTyrSerValThrLeuAlaArgLeuArgGlyAlaArgTrpGlySerGlyArg

        910                   930                   950
CACGGGGCGCGGGTGGGCCGGCTGGTGAGCGCCATCGTGCTTGCCTTCGGCTTGCTCTGG
HisGlyAlaArgValGlyArgLeuValSerAlaIleValLeuAlaPheGlyLeuLeuTrp

        970                   990                  1010
GCCCCCTACCACGCAGTCAACCTTCTGCAGGCGGTCGCAGCGCTGGCTCCACCGGAAGGG
AlaProTyrHisAlaValAsnLeuLeuGlnAlaValAlaAlaLeuAlaProProGluGly

       1030                  1050                  1070
GCCTTGGCGAAGCTGGGCGGAGCCGGCCAGGCGGCGCGAGCGGGAACTACGGCCTTGGCC
AlaLeuAlaLysLeuGlyGlyAlaGlyGlnAlaAlaArgAlaGlyThrThrAlaLeuAla

       1090                  1110                  1130
TTCTTCAGTTCTAGCGTCAACCCGGTGCTCTACGTCTTCACCGCTGGAGATCTGCTGCCC
PhePheSerSerSerValAsnProValLeuTyrValPheThrAlaGlyAspLeuLeuPro

       1150                  1170                  1190
CGGGCAGGTCCCCGTTTCCTCACGCGGCTCTTCGAAGGCTCTGGGGAGGCCCGAGGGGGC
ArgAlaGlyProArgPheLeuThrArgLeuPheGluGlySerGlyGluAlaArgGlyGly

       1210                  1230                  1250
GGCCGCTCTAGGGAAGGGACCATGGAGCTCCGAACTACCCCTCAGCTGAAAGTGGTGGGG
GlyArgSerArgGluGlyThrMetGluLeuArgThrThrProGlnLeuLysValValGly

       1270                  1290                  1310
CAGGGCCGCGGCAATGGAGACCCGGGGGGGTGGGATGGAGAAGGACGGTCCGGAATGGGAC
GlnGlyArgGlyAsnGlyAspProGlyGlyGlyMetGluLysAspGlyProGluTrpAsp

       1330                  1350                  1370
CTTTGACAGCAGACCCTACAACCTGCTGCCCTTCCCTGTCCCTTTCCACCCCCACCCAC
Leu

       1390                  1410                  1430
CCTCCAGAGGTCAGTGTTCTGGGACATTTGGGGACCCTTCTTTGACTAGAGTTTGGATCT
```

```
     1510                  1530                  1550
TGAGGGTGGTGATGGTCCCTGTTAAGGACTATTGTGTGCTTGCAAGTTG
```
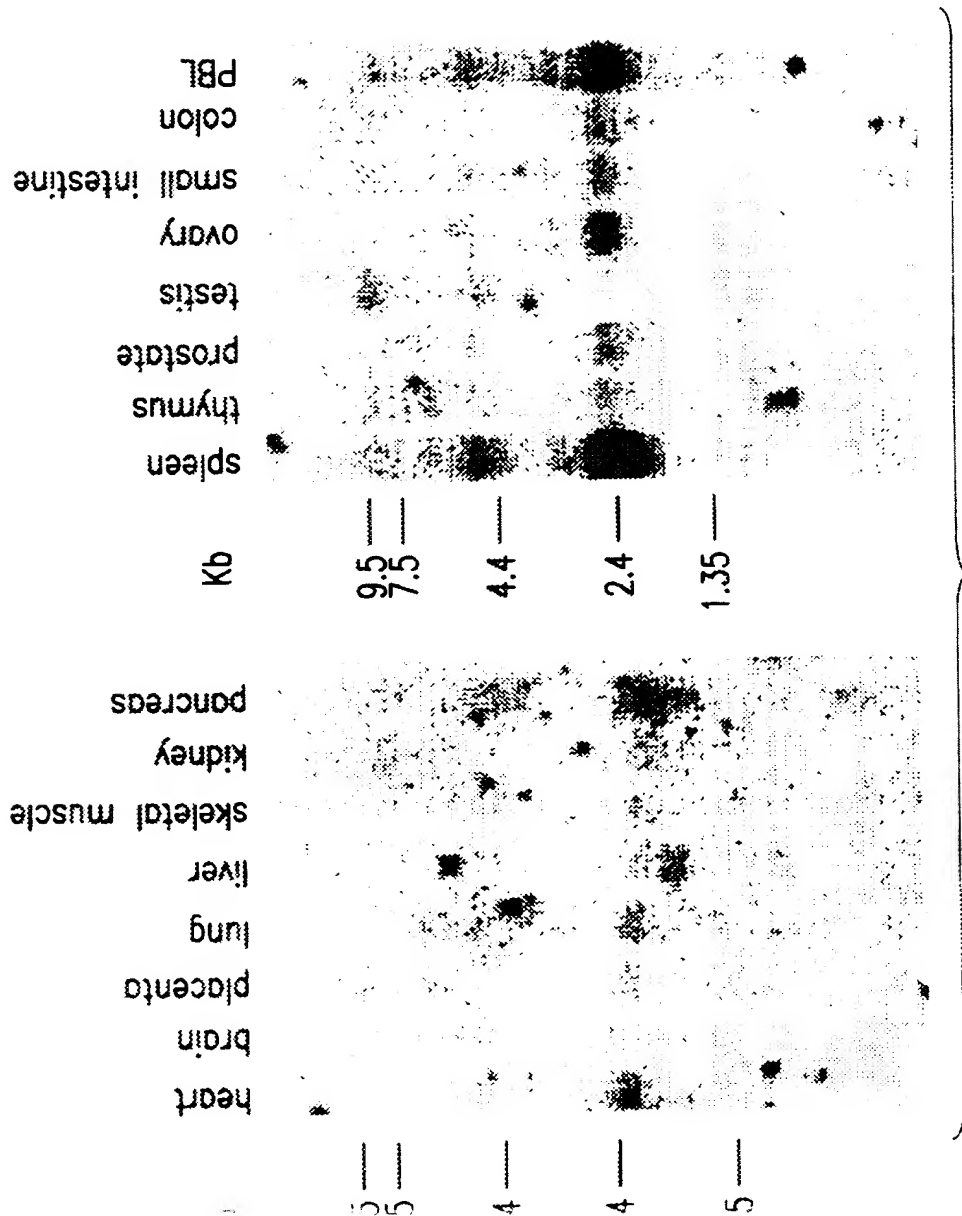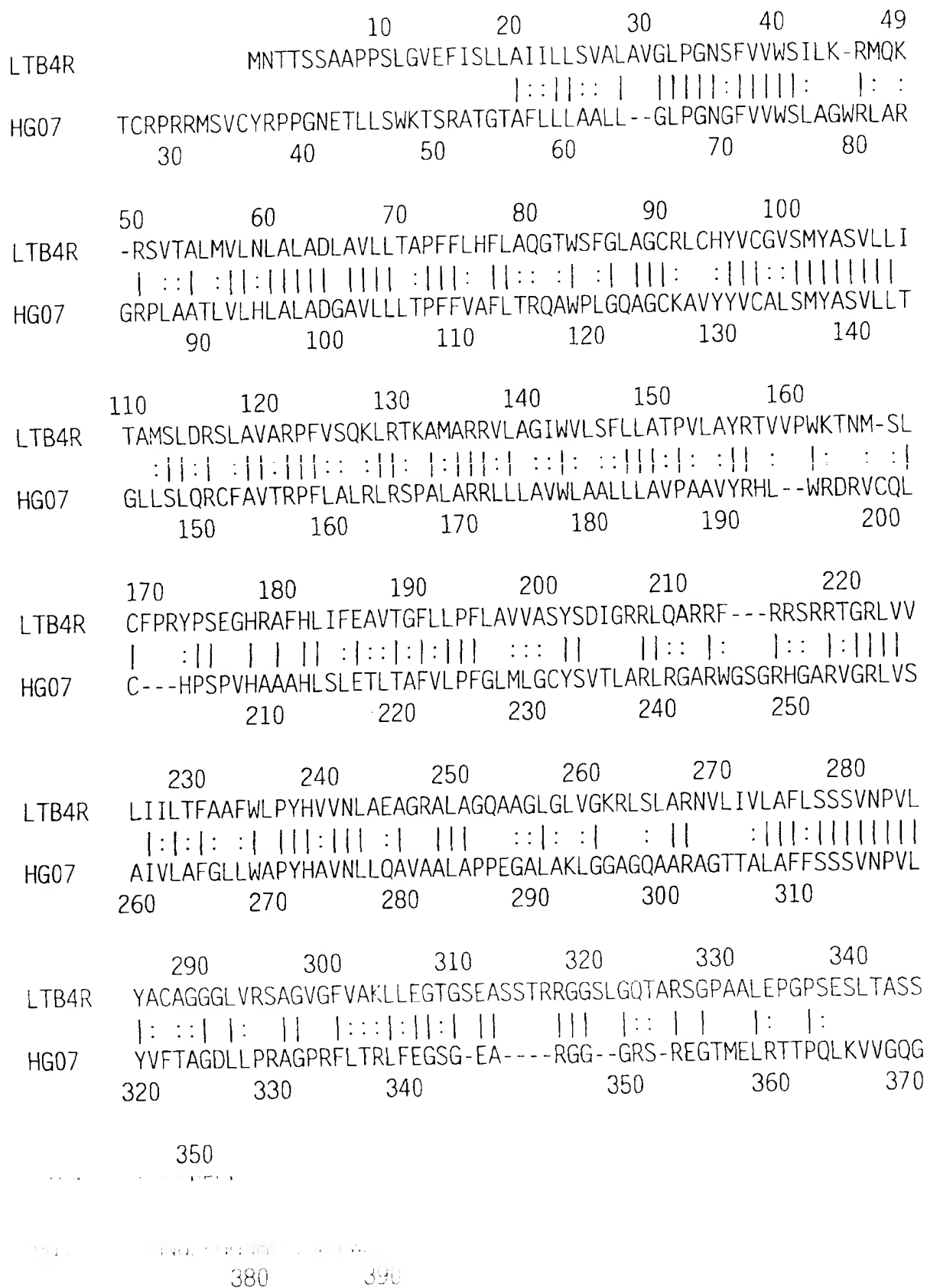
FIG.3B

FIG.4

```
                  10        20        30        40      49
LTB4R     MNTTSSAAPPSLGVEFISLLAIILLSVALAVGLPGNSFVVWSILK-RMQK
                 |::||:: | |||||:|||||:    |: :
HG07    TCRPRRMSVCYRPPGNETLLSWKTSRATGTAFLLLAALL--GLPGNGFVVWSLAGWRLAR
               30        40        50        60        70        80


                  50        60        70        80        90       100
LTB4R     -RSVTALMVLNLALADLAVLLTAPFFLHFLAQGTWSFGLAGCRLCHYVCGVSMYASVLLI
               | ::| :||:||||| |||| :|||: ||:: :| :| |||:  :|||::||||||||
HG07      GRPLAATLVLHLALADGAVLLLTPFFVAFLTRQAWPLGQAGCKAVYYVCALSMYASVLLT
                    90       100       110       120       130       140


                 110       120       130       140       150       160
LTB4R     TAMSLDRSLAVARPFVSQKLRTKAMARRVLAGIWVLSFLLATPVLAYRTVVPWKTNM-SL
               :||:| :||:|||:: :||: |:|||:| ::|: ::|||:|: :|| :  |:  : :|
HG07      GLLSLQRCFAVTRPFLALRLRSPALARRLLLAVWLAALLLAVPAAVYRHL--WRDRVCQL
                    150       160       170       180       190       200


                 170       180       190       200       210       220
LTB4R     CFPRYPSEGHRAFHLIFEAVTGFLLPFLAVVASYSDIGRRLQARRF---RRSRRTGRLVV
               |   :||  | | ||  :|::|:|:|||  ::: ||    ||:: |:  |:: |:||||
HG07      C---HPSPVHAAAHLSLETLTAFVLPFGLMLGCYSVTLARLRGARWGSGRHGARVGRLVS
                    210       220       230       240       250


                 230       240       250       260       270       280
LTB4R     LIILTFAAFWLPYHVVNLAEAGRALAGQAAGLGLVGKRLSLARNVLIVLAFLSSSVNPVL
               |:|:|: :| |||:||| :| ||     ::|: :|   : ||    :|||:||||||||
HG07      AIVLAFGLLWAPYHAVNLLQAVAALAPPEGALAKLGGAGQAARAGTTALAFFSSSVNPVL
               260       270       280       290       300       310


                 290       300       310       320       330       340
LTB4R     YACAGGGLVRSAGVGFVAKLLEGTGSEASSTRRGGSLGQTARSGPAALEPGPSESLTASS
               |: ::| | |:  ||  |:::|:||:| ||   ||| |:: | |   |: :|:
HG07      YVFTAGDLLPRAGPRFLTRLFEGSG-EA----RGG--GRS-REGTMELRTTPQLKVVGQG
               320       330       340          350       360       370


                350
```

FIG.5